AMENDMENTS TO THE SPECIFICATION:

Please insert into the specification under the BRIEF DESCRIPTION OF THE DRAWINGS and before the paragraph starting on line 28, page 11, the following paragraph:

The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the U.S. Patent and Trademark Office upon request and payment of the necessary fee.

Please substitute the paragraph on page 11, lines 28-32, continuing onto page 12, lines 1-15 with the following amended paragraph:

Figures 1A-1B depict an alignment of protein sequence homology. Figure 1A-1B depicts the Sequence alignment of PTB domains of the SNT and IRS proteins. Amino acid sequence identifiers (SEQ ID NOs: 8-33) and accession numbers of the proteins are indicated along the protein sequences. Protein sequences of FRS2α and FRS2β have been reported [Ong *et al.*, *Mol.Cell.Biol.* **20**:979-989 (2000)]. The experimentally determined secondary structure elements are displayed above or below the sequences of the PTB domains of SNTs or IRSs [Zhou *et al.*, *Nat. Struc, Biol.* **3**:388-393 (1996)], respectively. Asterisks highlight residues in the SNT-1 PTB domain that show intermolecular NOEs to the hFGFR1 peptide. Absolutely or highly conserved residues among the SNT and IRS PTB domains are shown in red and blue, respectively. Two underlined Arg residues of SNT-1 were both changed by site-directed mutagenesis to Gln. Arrows indicate constructs used in truncation analysis of SNT-1 PTB domain binding to hFGFR1 or TRK. Pro residues located C-terminal to the SNT-1 PTB domain are shown in bold. Figure 1B depicts the Sequence alignment of the juxtamembrane region of the FGFR family. For each FGFR group (FGFR1-4), protein sequences from three representative species, *i.e.*, human, mouse, and xenopus, are selected. The number of observed intermolecular NOEs identified for a particular amino acid residue of the hFGFR1 peptide is shown in red above the sequence. Absolutely or highly conserved residues are highlighted in yellow and blue background, respectively.

Please insert the Substitute Sequence Listing enclosed herewith in place of the Sequence Listing submitted on September 24, 2002.